


```
LLANGESTGNSGSSGSGGATGSSQTSISGDVVEACCSVLMSVACADPVVYKVAALKTLRLAMLVTPC
|||||
LLANGESTGNSGSSGSGGATGSSQTSISGDVVEACCSVLMSVACADPVVYKVAALKTLRLAMLVTPC
580 590 600 610 620 630 640
HSLAERIKLORLPVVDITLVKCADANSTLSLSLLELCKGAGELAVGREILKAGSIGIGGVYVLN
|||||
HSLAERIKLORLPVVDITLVKCADANSTLSLSLLELCKGAGELAVGREILKAGSIGIGGVYVLN
650 660 670 680 690 700 710 720
CILGNQTESNNWQBLLELCLIDRLLEFAEFVPHIVSTDVSOAEFVEIRYKLLSLTLFALQSIDNSHSM
|||||
CILGNQTESNNWQBLLELCLIDRLLEFAEFVPHIVSTDVSOAEFVEIRYKLLSLTLFALQSIDNSHSM
730 740 750 760 770 780 790
VGKLSRIYILSSARMVTVPHVFSKLEMLSVSSVSTHFTMRRLMAYADEVEIAEAIQLGVEDTLORQOH
|||||
VGKLSRIYILSSARMVTVPHVFSKLEMLSVSSVSTHFTMRRLMAYADEVEIAEAIQLGVEDTLORQOH
800 810 820 830 840 850 860
NSFCRHLFPPTIMQPTVPLECTVHLEKTKGKLCATKLSASSEDISERLARISVGSSSTTTTTTTEQPK
|||||
NSFCRHLFPPTIMQPTVPLECTVHLEKTKGKLCATKLSASSEDISERLARISVGSSSTTTTTTTEQPK
870 880 890 900 910 920 930
PMVQTKGRPHSQCLNSPLSHSOLMPALSTPSSSTPSVPAGTATDVSKHRLQGFIPCHIPSASPTQKRF
|||||
PMVQTKGRPHSQCLNSPLSHSOLMPALSTPSSSTPSVPAGTATDVSKHRLQGFIPCHIPSASPTQKRF
940 950 960 970 980 990 1000
SLOFHRNCPENKSDKLSPVFTQSRPLPSSNIHRPKSRPTPGNTSKQDPSKNSMTLDLNSKCDSDSFL
|||||
SLOFHRNCPENKSDKLSPVFTQSRPLPSSNIHRPKSRPTPGNTSKQDPSKNSMTLDLNSKCDSDSFL
1010 1020 1030 1040 1050 1060 1070 1080
SSNSNCCYTSDETVFTVEEKRCLDVNTLNSSTLLEASMPSSDTTVTFKSEVAVLSPEKAENDTYKD
|||||
SSNSNCCYTSDETVFTVEEKRCLDVNTLNSSTLLEASMPSSDTTVTFKSEVAVLSPEKAENDTYKD
1090 1100 1110 1120 1130 1140 1150
DYNHOKCKEKMEAEAEALAIAMASQVALPIVPOLOQVENGEDIIIOQDTPETLPCHTAKQPYREDT
|||||
DYNHOKCKEKMEAEAEALAIAMASQVALPIVPOLOQVENGEDIIIOQDTPETLPCHTAKQPYREDT
1160 1170 1180 1190 1200 1210 1220
EVLKQOQIGLGFSSCYQAQDGTGLMAVKQVTVYRNTSSEQVEVVEALREEMHMLNHPNIIIRMLGAT
|||||
EVLKQOQIGLGFSSCYQAQDGTGLMAVKQVTVYRNTSSEQVEVVEALREEMHMLNHPNIIIRMLGAT
1230 1240 1250 1260 1270 1280 1290
CEKSNYNLFIEWMAGSVAHLISKYGAFKESVWINYTEQLLGLSYLHENQIIHRDVKGANLLIDSTGQRLR
|||||
CEKSNYNLFIEWMAGSVAHLISKYGAFKESVWINYTEQLLGLSYLHENQIIHRDVKGANLLIDSTGQRLR
1300 1310 1320 1330 1340 1350 1360
IADFGAARFLASKGTGAGFQQLLGTATFMAPEVLRQOQYGRSCDVWSGCAIIEMACAPPNWAEKSHNH
|||||
IADFGAARFLASKGTGAGFQQLLGTATFMAPEVLRQOQYGRSCDVWSGCAIIEMACAPPNWAEKSHNH
1370 1380 1390 1400 1410 1420 1430 1440
LALIFKIASATTAPSIPLSHSPGLRDVALRCLELQPODRPPSRELLKHPVFTTW
|||||
LALIFKIASATTAPSIPLSHSPGLRDVALRCLELQPODRPPSRELLKHPVFTTW
1450 1460 1470 1480 1490 X
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|||||
LALIFKIASATTAPSIPLSHSPGLRDVALRCLELQPODRPPSRELLKHPVFTTWXLIQINIVETGCSRE
1450 1460 1470 1480 1490 X 1500 1510
KKLVGNHIDIYCHDATEQLXTRPVGNPYLSMXL
1520 1530 1540
2. US-09-697-898-3 (1-1495)
US-09-359-756-1 Sequence 1, Application US/09359756
Initial Score = 16 Optimized Score = 53 Significance = -0.40
Residue Identity = 23% Matches = 81 Mismatches = 130
Gaps = 139 Conservative Substitutions = 0
Translation Frame = 4
X 10 20
PSPEAGGGGALKASSARAAAA
PSPEAGGGGALKASSARAAAA
1260 1270 1280 1290 1300 X 1310 1320
LLQSGKXALSAASTVMPASLCXHGGLFQGYMVRSHLVKGLFGVXVCHSEKA---LGKLFSLLELLELI
1330 1340 1350 1360 1370 1380 1390
GLLRAGSGGRERADWRRLQRLK---VRSVELDQI-----PEQLFLA-ASPP---AS-----
30 40 50 60
SLCDLMGS-CQEKDCVGLMKLVKPHLPGLLETQLLSDSFQIHLXGLVLPPQALAYFSPTIRASPLAYR
1330 1340 1350 1360 1370 1380 1390
--STSP-SPEPADAAGSGTGFPVAVPPPHGAASRRG-AHLTESVAAP-----DSGASSPA--AAEPG
70 80 90 100 110 120
LFSVPXSPVPLDDHPSCATLXEFLYSPSH---DRGQLQETARRRASPAPRRLDRSRRCAPPPTRXG
1400 1410 1420 1430 1440 1450 1460
GRRR-GWELRGHAAAPPOAGSRSHSL-----RP-----RAPATGKSRPPA-----VRQGRAAAQA
1470 1480 1490 1500 1510
190 200 210 220 230 240 250 260
-GPVVVVKPIPVKGDGSEMHLAAESPGEVQASASPAGSKRRSPSGNSPGRVTVKSESFGVRRKRVSPVFF
AGP-----APHSALCAAAAASPPARGPRCPPP-----AAVPR
1520 1530 1540
QSGRIPTPPRAPSPDGFSPSYSPETNRRVKNVKNRRLVLLQOIGPNSFLIGDSDPNKIRVFIGPQNCSCAH
270 280 290 300 310 320 330
Q-----PPARCSPXG-----LIRR-----RLPQG
1550 1560 X
GTFCIHLLFVMLRVFQLE
340 350
```

3. US-09-697-898-3 (1-1495)
US-09-359-756-1 Sequence 1, Application US/09359756

Initial Score = 14 Optimized Score = 56 Significance = -0.40
Residue Identity = 26% Matches = 72 Mismatches = 133
Gaps = 68 Conservative Substitutions = 0
Translation Frame = 6
X 10 20
PSPEAGGGG--GALKASSARAA
LTRRFVSSGLYGEKPSGEGALRGGVILPLXKGTGETFLTLTPGSDFTVVRPQGLPGEGLRPLEAGEAALA
1280 1290 1300 1310 1320 X 1330 1340
-----AAGLLREAGS---GGRERADWRRLQRLKRVSVELDQLEPQLFLAASPPASTSPS-----
30 40 50 60 70
|||||

WTSPGDSAAKFIPIIDPSPLTIGITGTTGPRFLILNHS--CFQAGIQVAFSFLIIRSSGSSILCNPLRVS
 1350 1360 1370 1380 1390 1400 1410
 ----PEPADAAGSGTGFPQVAVPPPHGAASRRGAHLTESVAAPDS--CASSPAAAECEKRAPEESP-AA
 80 90 100 110 120 130
 LFSISRPAAG--AGDGAAGARFSGSAAGLEAPL--SGAATSVKAPRRLAAPWGGGTATGKVPPLPA
 1420 1430 1440 1450 1460 1470 1480
 140 150 160 170 180 190 200 210
 APAGEMENKETLGLHOMDORPEERMIREKLKATCMPAWHEMLERENRRGPPVVVKPIPVKGDGSEMHLA
 ASAG-----SGDGEVEAGGEAARKSCGSGSSSTL-RTLR-----SCRRRQS
 1490 1500 1510 1520
 220 230 240 250 260 270
 AEPGEVQASAAASPASKR-----RSPSPGNSPGRVTYKSESPGVRRKRVSPVFPQSGRITPPRRAPSPDGF
 ARSRPPLPASRSSPAAARALALALAP-PPPPASG
 1530 1540 1550 1560 X
 280 290
 SPYSPETNRRVN

4. US-09-697-898-3 (1-1495)
 US-09-359-756-1 Sequence 1, Application US/09359756

Initial Score = 9 Optimized Score = 246 Significance = -0.41
 Residue Identity = 21% Matches = 374 Mismatches = 846
 Gaps = 559 Conservative Substitutions = 0
 Translation Frame = 3

X
 PSPE-----AGGGGALKAGSARAAAGLLREAGSGRRERADWRRRL-----
 10 20 30 40
 EPXGRRRRSPQEQPARCGRCTAAGGGRGPRAGGLAAGAAQAEGCAGPAAAXAALPCELTAGLADFPV
 10 20 30 40 50 60 70
 50 60 70 80 90 100 110
 --RKVASVELDQLEQPLFLAASPASSTSPSPADAGSGTGFPVAVPPPHGAASRRGAHLTESVAAPD
 AGARGSGEWDRLP--ACGGAAP--RSQPARRPPYRVGGGAG--QRRLESRSGRA--RGAGARRRAVSC
 80 90 100 110 120 130
 120 130 140 150 160 170 180
 SGASSPAAAEPPGEKRAAPAPAPAG-----REMEKETLGLHMDRPEERMIREKLKATCMPAWKE
 SG--PRRSXDGEXR-----NSQVADQKSGSRGTNDQGETGNL--YASLEARM-VGKEKXARACGKTN
 140 150 160 170 180 190
 190 200 210 220 230 240
 WLRR-----NRRGP-VVVKPIPVKGDGSEMHLAAESPGVQASAAASPASKRRSPSPGNSPSGR
 PSXRRWIXNESLSSXVSRGPGKCGFTSFQRTQSFQSWQLPIRSHSEIRIS-----RSKEKKSFPFAFSEWQN
 200 210 220 230 240 250 260
 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420
 TVKSESPGVR-----RKRVSPPVFGS-----GRITPPRA-PSPDGFSYSPEETNRR-----VNKMPRA-R
 HTTPKSPFTFWLLTIXPGNKPCQSDAGQTLTAADRAXLFPD-----WRRQPRQXIFGVYWASE
 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420
 LYLLOIGFNSPLIGDPSPNKTRVFIGPQNCSCAGTFCIHLLFWMLRVFQLEPSDPMWLKTLK-----
 LQLCTWNILYSSAI-CDAPGVSTRTT-RPNVMKNTKEF-XGXEFEV-----PEIS-----QXAXLKQSSIS
 330 340 350 360 370 380 390 400 410 420
 --NFEVESLPQKYHSRSPRIKAPSNTI-----QKFSVRMSNSHTLSSSTSTSSSENSIKDEEQMCPICL
 XHHEVCVTHVK-----FSIVIIYPIYIXRQKHGXRGTDVSVLLVGHAXXKRSYVARRLQEQAP-----

390 400 410 420 430 440
 430 440 450 460 470 480
 LGMDBESTVCEDEGCR--NKLHHCMS--IWAE-----ECRRNREPLICPCRSKRWASHDYFISH
 ----PLHV-NLGRVVKXKRTFNMSPLIXVEISXFLQPRVVKSCGFPFPFQSCCTAANRTAAAFGWITK
 450 460 470 480 490 500 510
 490 500 510 520 530 540
 ELSPVDSPSSL-RAAQOQTVQOQPLA-----GSR-RQESNENLTHYGTQ-----QIPAYKDLAEPW
 E-SREOFXFPYLSWNSNAPSCLOFAXMDSGVWNGTRWLLIFXKLECEDRDGPASFPXQWGPFAVGKWEHW
 520 530 540 550 560 570 580
 550 560 570 580 590
 IQVFGMELVCLFSRWNVNREMLRR-----LSHDV-----SGALLANGESTGNSGSSGSSPSG-G
 KFGQOQWQPEWGSOWVFPDQVLRRCGGMLQRSVNGLCXPCQLQVRCFCFNIES--HAGIYSLPQFGKN
 590 600 610 620 630 640 650
 600 610 620 630 640 650
 ATSGSSQTSISGDVVEAC--CSVLSWV-----CADPVYKYVAALKTLRAMLVYTPC-----HSLAE
 QTSETSPASCRHHPSPQWRCQCPHKSAAVHINTVGTQVORSPRRVSGVSHQRTKSWIHHYWWXCLCLKLYSNKPN
 660 670 680 690 700 710 720
 660 670 680 690 700 710 720
 RIK-LQRLQOP-----VV-----DTILVKCADANSRTSLS-STLELCKGQAGELAVGREILKAGSIGIGG
 XIKQARTSPPLSYXATVVGISXIL-----SSYCOYXCF--SKACXNOYKAAVPLNLCA-----VH
 730 740 750 760 770 780
 720 730 740 750 760 770 780
 VDVYVNCILNGQTESNNWQELLGRCLIDRELLLEFAEFY--PHIVSTDVSOAEPVEIRYKLLSLTLTFALQ
 XXPELN--GWQT--FOKDL--800 810 820 830
 790 800 810 820 830 840
 SIDNSHSMVGKLSRIYLSARVMT-----VPHVFSKLEMLSVSS--VSTHTFRMRRLMAVADE---L
 SPFDGLCRXGNGCRSHPVGRRRRTTTTQQLQASVPNNYLETNNSPFXVHSPRENWKRIMCYKIECQF
 840 850 860 870 880 890 900
 850 860 870 880 890 900
 -VEIAEAIQ-----LGVEDT-----LQOQHNSPCRHL-----FP--TTIWKPORTVP---L
 910 920 930 940 950 960 970
 RGHFXTGQDFSRFTFXFNNNNNNNRATKANGSNKRQTPOSVFELLSSFISFFINVSLLYNPFFYFICTSW
 910 920 930 940 950 960 970
 890 900 910 920 930 940 950 960 970 980 990
 ECTVHLEKTGKG--LCAT-----KLS-----ASSEDISERLA-----RISVGP-
 980 990 1000 1010 1020 1030 1040 1050
 HCNRLXAXTSGIHSLQNTFCISSNTAQVFTTIPQKLSXKQRLXRTPPSLYSVKTLALQHTQAKALSTYPR
 980 990 1000 1010 1020 1030 1040 1050
 ----SSSTTTTTTTEOKPM-----VOIKGRPHSCLNSSLPLS-----HHSQMFALPS----
 XYKXTGSLKXKHDTXGEQFQWXXQLWLSQXXLLLYQXRDVSHPSRGEMQIRCOYRAQLQXGSPXSIIY
 1060 1070 1080 1090 1100 1110 1120
 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120
 ----TPSSSTSPVPAG-----TATDVSK-HRLQG-----FIPC--RIPSASP-----QTQK
 AFKYNNSFPYRSCCPVSXKXKXXYLQRCESXSKVQREDGXYRRRSFNCNCHNVSVSGSPHSSSAAGKX
 1130 1140 1150 1160 1170 1180 1190
 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190
 FSLQFHRNCPENKSDKLSVPFT-----QSRPLPSNIHRPSPRPTPGNTSKQGDPSKNSMTLDLN
 WRRVHHYSTGTTRDSTRYQSKTTVXRHHXMAERSTDRPKSIFELLSSGR--CQNMVNG-----XTGDL-
 1200 1210 1220 1230 1240 1250

1070 1080 1090 1100 1110 1120
SSKCDSDSFGLSNSNCCYTSDETVTPVE-EKCRLDV-----NTEINS-----SIEDLLE
-CQKHIFXARRSRSTKRRDNDE-----PSESSKHDXDVGSVHYEQLOSLSXMDGRG-GGSFAEXINSLQR
1260 1270 1280 1290 1300 1310 1320
1130 1140 1150 1160 1170 1180 1190
ASMPSSDTTTFKSEVAVLSPERAENDDTYKDDVNNOKCKEVEA--EEBEALAJAMASASOVALPIVPO
ISSYXLHXITVPTFTV---SPXK-----PMSQRCQCFANXQHWSETKNCRCFWSCSQVGIKRNWC
1330 1340 1350 1360 1370 1380
1200 1210 1220 1230 1240
LOVENGEDIIIIQQDTPETLPHTKAKQPYRE---DTEMLKGOQIGL-----GAFSSC-----Y
RRV-----SCTITGDCNIYCTGKTSVWKELXCMECMLCYVENGGLCKTMECRKTLOSSCFDIXDCXNY
1390 1400 1410 1420 1430 1440 1450
1250 1260 1270 1280 1290 1300 1310
QAQDVGTGLMAVQVTVYRNTSEOEVEALREIRMMHNLNHIIRMLGATCEKSNYNLFIEWMAGGS
CSIDPFT---FVSWFT---RCGSS-----LFRSTSGQTSIKR---AT-EAS-----S
1460 1470 1480
1320 1330 1340 1350 1360 1370 1380
VAHLLSKYAFKESVINYTEQLRLGLSYLHENQI IHRDVKGANLIDISTGQRLRIADFGAARLASKGTGA
-----LSYV-----MVANYTDQLRR-----NRLNKRKK-----TCGEPHYXLYRXPCHXTAMNEAS-----
1490 1500 1510 1520 1530
1390 1400 1410 1420 1430 1440 1450
GEFGQGLGTIAFMAPVLGQQVGRSCDVNSGCAIIEMACAPWNAEKHNHLALFKIASATAPISIP
GE-----PLPKYVIDKSXSV-----PKLSMOK-----PKLVOK-----X
1540 1550
1460 1470 1480 1490
SHLSPGLRDVALRCLELQPDPRPSRELLKHPVPTTW

5. US-09-697-898-3 (1-1495)
US-09-359-756-1 Sequence 1, Application US/09359756

Initial Score = 9 Optimized Score = 50 Significance = -0.41
Residue Identity = 22% Matches = 76 Mismatches = 153
Caps = 116 Conservative Substitutions = 0
Translation Frame= 5
X 10 20
PSPEAGGGGALKASARAAAA
TAAVLKPKHPVFTVWAVSSNQERVRPVLLOXVOSGPHFVNTAVCFRLAIWKEAIWXRG-----SSGWCDSA
1240 1250 1260 1270 1280 1290 1300
30 40 50 60 70
GLLREAG---SGGRER-----ADRRRLQRLKVRVSELDQLPEQFLFLAAGPPAS-----STS-----
TLKRWGNSFPFVSWRFXPHCATKXGVARRTAFAGSWXSRTCLDL--SWRLSCXVIHFRSISFNWDFYH
1310 1320 1330 1340 1350 1360 1370
80 90 100 110 120
---PSP---EPADAGSGTG---FQP-----VAVPPHGAASRRGAHLTESVAAPDSGASSPAAAPPG
HRPSPISPPFVLPFGWHTGCLQLPDHSFLWTIHLVOP---PESFFILHLTTGGRCRRRLGGGRPLLPFG
1380 1390 1400 1410 1420 1430 1440
130 140 150 160 170 180
EKR---APAA-----EPSPAAAPAGRENMENKTLKGLHKMDRDRPEERMIREKLCATCMPAKHWELERRNR
LGRCTRGAAVRRRLKGVGAAPAG-----GSGVRRHRLKAGPTP--RCVRLGLRRRGS
1450 1460 1470 1480 1490

190 200 210 220 230 240 250 260
RGPVVVKPIPVKGDGSEMMHLAABSPGEVQASAAASPASKGRRSPSPGNSPGRVTKSESGVRRKRVSPVPF
RG-----GRRXGKGERLL-----ROLVOLHTPHFA-----QLPPPPVRP-----LAAFAAR-----LPO
1500 1510 1520 1530 1540
270 280 290 300 310 320 330
QSGRITPPRAPSPDGFSPSPYSPETNRVNVKVMRARIYLLQIQIPNSFLIGGSDPNKYRVFIGPQNCSCAH
QS-RGSR-ARAARLEGSS-----AAACLEFA
1550 1560 X
340
GTFCIHLLFVMLR

6. US-09-697-898-3 (1-1495)
US-09-359-756-1 Sequence 1, Application US/09359756

Initial Score = 9 Optimized Score = 251 Significance = -0.41
Residue Identity = 20% Matches = 359 Mismatches = 911
Caps = 456 Conservative Substitutions = 0
Translation Frame= 2
X 10 20 30 40 50
PSPEAGGGGALKASARAAAAAGL-----LREAG--SG-----GREER-----DWERRQLRKVRVSELDQLPEQ
RALRQAAAEPSRRAACARLPRDCCGRRAAGAAAGRTGGGSCAKGCVGWSWTSCLSRSSSLPHRRPP
X 10 20 30 40 50 60
60 70 80 90 100 110 120
PLFLAASP-----PASSTSPSEPADAAGSGTGFPVAVPPPHGAASRRGAHLTESVAAPDSGASSPAA
ALPRRSPRTGCVGPASSLWRCRP-----TEPPAGAAPTLPSEWRRTAAP-----RVQORP
70 80 90 100 110 120
130 140 150 160 170 180
EPG-EKRAPAAEPSPAAAPAGRENMENKTLKGLHKMDRDRPEERMIREKLCATCMP-----AKHWELERRNR
SPGRSGRPPSLLQRPVVRWRIKLSKCTRWIVORNEXSGRNKRQVCPQCGSTNGKGBIGELMWX
130 140 150 160 170 180 190
190 200 210 220 230 240 250 260
GFPVVVKPIPVKGDGSEMMHLAABSPGEVQASAAASPASKGRRSP---SPGNSPGRVTKSESP-GVARKRV
NQSQLKEMDLK-XITXQLSLQERSROVRLHOLPKA-DAVLLATPHQVAXNQNLQEXGEKEFFQCLPRVAE
200 210 220 230 240 250 260
260 270 280 290 300
SPVP-----FQSGRI-----TPERRAPSPDGFSPSPYSPETNRVNVKVMRARIYLLQIQIPNSF
SHHPPEPLHQWASHHIALRKQTAVALTKXCGPDCTYCSRXGLTLXLEETAQTINTGCLLGLRTAAVHMS-
270 280 290 300 310 320 330
310 320 330 340 350 360 370 380 390
LIGGSDPNKYRVFIGPQNCSE---CAHGTFC-----IHLFVMLR---VFQLEPSDPLMRLKTNF--
-----VFICYLXSCGCFNXLQTCYGEKLRILRLRVCSRNITVGVAAQSKLHLVTPSRSLFHA
340 350 360 370 380 390
-----EVESLFOKVHRS--RSSRIKAPSRNTICKFVRSNNSHTLSSSTSTSSSENSIKDEBEQMC
400 410 420 430 440 450 460
COILIHCHHLVLLHLVQKTAHWRNRCVLFACWACLWKV--LOCVKTAGTCTTTACQPGQKSVSE---
430 440 450 460 470 480 490
PCLLGLMLEDSEITVCEDCGRNKLHHHCMSIWAEECCRRNRREPLICPLCKRSKWRSHDFYSHELSSVDPSPSL
-IENL-----XYVPFVDLSGDLMISTATSC-----QVLIWPLPSELHSSKPYSS--SSLWLDHEGIK
470 480 490 500 510
500 510 520 530 540 550

RAAQOQTVOOQPLAGS-----RRNOESFNLTHTYQTOIPPAYKDLAPM-IQVFGMELVGCULFSF
RA--ILTLIMELSKSLTLTXILSHGPRCEWM--SLAAY-----FLETGMERNPSGVFPMMSVG-----P
520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160 5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280 5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400 5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520 5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640 5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760 5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880 5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240 6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360 6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480 6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600 6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720 6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840 6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960 6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080 7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200 7210 7220 7230 7240 7250 7260 7270 7280 7290 7300 7310 7320 7330 7340 7350 7360 7370 7380 7390 7400 7410 7420 7430 7440 7450 7460 7470 7480 7490 7500 7510 7520 7530 7540 7550 7560 7570 7580 7590 7600 7610 7620 7630 7640 7650 7660 7670 7680 7690 7700 7710 7720 7730 7740 7750 7760 7770 7780 7790 7800 7810 7820 7830 7840 7850 7860 7870 7880 7890 7900 7910 7920 7930 7940 7950 7960 7970 7980 7990 8000 8010 8020 8030 8040 8050 8060 8070 8080 8090 8100 8110 8120 8130 8140 8150 8160 8170 8180 8190 8200 8210 8220 8230 8240 8250 8260 8270 8280 8290 8300 8310 8320 8330 8340 8350 8360 8370 8380 8390 8400 8410 8420 8430 8440 8450 8460 8470 8480 8490 8500 8510 8520 8530 8540 8550 8560 8570 8580 8590 8600 8610 8620 8630 8640 865

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file 6168950 x 697898.res made by spaula on Thu 20 Feb 103 16:41:15-PST.

```
Query sequence being compared:US-09-359-756-1 (1-4693)
Number of sequences searched: 1
Number of scores above cutoff: 1
```

Results of the initial comparison of US-09-359-756-1 (1-4693) with:
File : US09697898mod.pep

Subject	Score
NUMERICS	167
OF	333
SEQUENCES	500
S	1499

Sequence Name	Description	Length	Score	Init. Opt.	Sig. Frame
1. US-09-697-898-3	Sequence 3, Application US	1495	1499	1499	0.00 1

1. US-09-359-756-1 (1-4693)
US-09-697-898-3 Sequence 3, Application US/09697898

Initial Score	=	1499	Optimized Score	=	1499	Significance	=	0.000
Residue Identity	=	100%	Matches	=	1495	Mismatches	=	0
Gaps	=	0	Conservative Substitutions	=	0			
Translation Frame	=	1						

X	10	20	30	40	50	60	70
PSPEAGGGGALKASARAAAAGLIREAGSGGREADWRRQLRKVSVELDQLPEOPLFLAASPASSTSP							
PSPEAGGGGALKASARAAAAGLIREAGSGGREADWRRQLRKVSVELDQLPEOPLFLAASPASSTSP							
X	10	20	30	40	50	60	70
80	90	100	110	120	130	140	
SPSPADAAAGSGTGFOQVAVPPHPHGAASRRGAHLTSTVAAPDGSASSPAAAEPEGKRAPEAEPSPAAAPAGRE							
SPSPADAAAGSGTGFOQVAVPPHPHGAASRRGAHLTSTVAAPDGSASSPAAAEPEGKRAPEAEPSPAAAPAGRE							
80	90	100	110	120	130	140	
150	160	170	180	190	200	210	
MENKETLKGHLKWDDEPEEREMIREKLKATCMPAKWHEMLERNRERGVPVVKPIPVKGDGSEMHLAAESGCE							
MENKETLKGHLKWDDEPEEREMIREKLKATCMPAKWHEMLERNRERGVPVVKPIPVKGDGSEMHLAAESGCE							
150	160	170	180	190	200	210	
220	230	240	250	260	270	280	
VQASAASPASKGRRSPSPGNSPGRVTKSESGVGRKRVSPVPFQSGRITTPPRAPSPDGFSPYSPBETNRR							
VQASAASPASKGRRSPSPGNSPGRVTKSESGVGRKRVSPVPFQSGRITTPPRAPSPDGFSPYSPBETNRR							
220	230	240	250	260	270	280	
290	300	310	320	330	340	350	360
VNKVNRARLYLLOQIGNSFLIGDSPDNKYRVFIGPQNCSCAHGTCIHLFLVMYLVFOLESPDMLMKRT							
VNKVNRARLYLLOQIGNSFLIGDSPDNKYRVFIGPQNCSCAHGTCIHLFLVMYLVFOLESPDMLMKRT							
290	300	310	320	330	340	350	360
370	380	390	400	410	420	430	
LKNFEVESLFQYHSRRSSRIKAPSNTLQKQFVSRMNSHTLSSSSTSTSSSENSIKDEEEMQCPICLLGML							
LKNFEVESLFQYHSRRSSRIKAPSNTLQKQFVSRMNSHTLSSSSTSTSSSENSIKDEEEMQCPICLLGML							
370	380	390	400	410	420	430	
440	450	460	470	480	490	500	
DEESLTVCEDCGRNKLHHCHMSIWAECRRNREPLICPLCRSKWSDHFSHELSSPVDSPSSIRAAQOQTV							
DEESLTVCEDCGRNKLHHCHMSIWAECRRNREPLICPLCRSKWSDHFSHELSSPVDSPSSIRAAQOQTV							
440	450	460	470	480	490	500	
510	520	530	540	550	560	570	
QOOPLAGSRNQEENFLTHYGTQOIPPAYKULABEWIOVFGMELVGLCFSRMNVRMALRRLSHDVS GAL							
QOOPLAGSRNQEENFLTHYGTQOIPPAYKULABEWIOVFGMELVGLCFSRMNVRMALRRLSHDVS GAL							
510	520	530	540	550	560	570	
580	590	600	610	620	630	640	
LIANGESTGNGSGSGSGSPGGATSGSSQTSIGDVEVACCSVLMSVADPVYKYVYVAALKTLRAMLYVTPC							
LIANGESTGNGSGSGSGSPGGATSGSSQTSIGDVEVACCSVLMSVADPVYKYVYVAALKTLRAMLYVTPC							
580	590	600	610	620	630	640	
650	660	670	680	690	700	710	720
HSLAERIKLORLQFPVDTILVKCADANSTLSQTSITLLECKQOAGELAVGREILKAGSIGIGGVYDLN							
HSLAERIKLORLQFPVDTILVKCADANSTLSQTSITLLECKQOAGELAVGREILKAGSIGIGGVYDLN							

NMNVREMA LRR LSHD VSGALL LANGE STNGGSSGSSPSGGATSGSSQTSISGDVVEAC-CSV--LSMVCVA
 550 570 580 590 600 610 620

-----TLLXGXEPWCYLLAVTKESNPFSSQLXTSXNVQMPAAQVSCPYQHWCNCA-----690
 680
 670
 660
 650
 640
 DPVYKVVAALKTLRAMLVYTPC--HSLA-----ERIKQLRLQP---VVDTI--LVKC-----A
 630 640 650 660 670

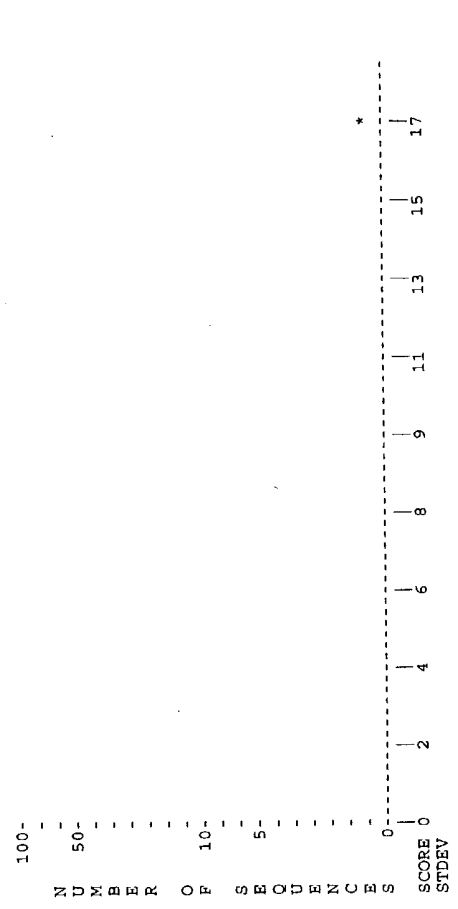
700 710 720 730 740 750
KAKQESWQLAEKYKLDPLVVLVMSXVVFETKQO---TICKNFLAFLVXIDCCWNFLNFIILISV
| | | | |
DANERTSOL-----SITLELCKGAGELAVGREILKAGSIGI-CGVDPVINCILGNOT
680 690 700 710 720

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.
1. US-09-697-898-3	Sequence 3, Application US	1495	10	263
1. US-09-359-756-1 (1-4693)				
US-09-697-898-3	Sequence 3, Application US/09697898			
Initial Score = 10	Optimized Score = 253	Significance = 0.00		
Residue Identity = 21%	Matches = 374	Mismatches = 846		
Gaps = 559	Conservative Substitutions = 0			
Translation Frame = 3				
10	20	30	40	50
EPXRRRRRSPQGEQARGCRTAAGSGQRPRAGGLAAQAASQAFSGAGPAAKAAALPCRLTAGLDFPV				
PSFE-----ACGGGALKASSARAAAAGLLRAGSGGRERADWRRLQ-----				
X		10	20	30
80	90	100	110	120
AGARGSGEWDRLF--ACGGAAP--RSROPARRPPYRVGGAG--QRLESRSGR---RGEAGARRAVSC				
--RKRSVELDQLPEQPLFLAASPASSTSPSPEDAADSGTGTFQVAVPPPHGAASRRGAHLTESVAAPD				
50	60	70	80	90
140	150	160	170	180
SG---PRRSVDGEXR-----NSQVADGXSRRTNDOGETEGL---YASLEARM-VGKEKXARACGGKTN				
SGASSPAAAEFGKRAPAAAPFSPAAPAG---REMNKETLKLHWRDDRPERMIREKLKATCMPAWKHE				
120	130	140	150	160
200	210	220	230	240
PSYRRWIXNSLSXVSRGPKCGFTSFQPTQSFNQWLPPIRSHSIRIS---RSKEKXSPSPASEWQN				
WLERR-----NRRGP-VVVKPIPVKGDSENMHLAAESPGEVQASAAASPKRRRSPSPGNSPSGR				
190	200	210	220	230
270	280	290	300	310
HTTPKSPFTRWLLTIXPKGNPKPCQSDAGQTVLTADRAXLFPD-----WRRQPROXIPGVYWASE				
TVKSESQVR-----RKRVSPVFQS---GR-TIPERRA-PSPDGFSPPSPETNRR-----VNKMVRA-R				
250	260	270	280	290
330	340	350	360	370
LQLCTWNLXSSAI-CDAPGVSTRTF-RPNVMEKNFEB-XGXEYF-----PRIS---QXAXLKQOSSIS				
LYLLQIQIPNSFLIGGSDPSDNKYRVFIQPCQSCAAGTFCIHLFLVMLRVFQLPSPDMLWKRLK-----				
300	310	320	330	340
390	400	410	420	430
XHHPEVCFTHVK-----FSYIVIIYFIYFKRQKHGARGTDVSYLLVGHAXXKRSYSVXRRLQEQAAP----				
--NPEVESLFQKYSRSSRIKAPSRNTI---QKFVSRMGNSHTLSSSTSSSENSIKDEEBQMCPICL				
370	380	390	400	410
450	460	470	480	490
-----PLHV-NLGRYVKKXRTFNMSPLXIXVEISAFLOPRVVKSCGFFFPQSCATAANRTAAAPGWITK				
LGMLDESLTVCEDGCR--NKLHHHCNG--IWAE-----ECRRNREPLICPLCRSKWRSHDFYSH				
430	440	450	460	470
520	530	540	550	560
E-SREQXPYSLWMSANPCLQRFESXAMDGVMWNGTRWLLTFXKLECEDRGDQFASFPXQMGPAVKWGEHW				
ELSSPVDSPSSL-RAAQOQTVOQOLA-----GSR-RNQESENELTHYGTQ-----QTPPAYKDLAEFP				
490	500	510	520	530
590	600	610	620	630
KFWGQWQKQPEWGHWVFPDQYLRRCGGMLQRSGVNGLCXPCLOASVCCCFKNIES--HAGIYSLPQSGKN				

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> O <
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4
Results file 6168950_x_697898.res made by spaula on Thu 20 Feb 103 16:42:08-EST.
Query sequence being compared:US-09-359-756-1 (1-4693)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-359-756-1 (1-4693) with:
File : US09697898mod.pep



PARAMETERS			
Similarity matrix	Unitary	K-tuple	2
Translation frame	6		
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	500
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		

SEARCH STATISTICS			
Scores:	Mean	Median	Standard Deviation
	17	0	0.00
Times:	CPU		Total Elapsed
	00:00:00.00		00:00:00.00
Number of residues:			1495
Number of sequences searched:			1
Number of scores above cutoff:			1

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

1200 1210 1220 1230 1240
CSIDPFT---FVSWFT--RCGSS-----1470 1480
QAQDVGTGLMAVKQVTVYVNTSSQEEVVEALREIRMMSHLNHNIIIRMLGATCEKSNYNLFIEWMAGGS
1250 1260 1270 1280 1290 1300 1310
1490 1500 1510 1520 1530
-----LSYY-----MVANYTDQLRR-----NRMNKKK-----TCGEPHYLRXPCHXTAMNEAS-----
VAHLLSKYGAFKESVINYTEQLRLGLSYLHENOQIIHRDVKGANLLIDSTGQRLRIADFGAARLASKGTGA
1320 1330 1340 1350 1360 1370 1380
1540 1550 1560 X
-----PLPKYVIDKXSV-----PKLSMQK-----PKLVQK
GE-----
GEPQGLLTGTFMAPEVLRGQOYGRSCDWSVGCAIIEMACAKPPWNAEKSNHNLALIFKIASATTAPSIP
1390 1400 1410 1420 1430 1440 1450
SHLSPGLRDVALRCLELPQDRPPPSRELLKHPVFRITW
1460 1470 1480 1490

A 100% identical sequence to the query sequence was not found.

X	420	430	440	450	460
1	1	1	1	1	1
2	1	1	1	1	1
3	1	1	1	1	1
4	1	1	1	1	1
5	1	1	1	1	1
6	1	1	1	1	1
7	1	1	1	1	1
8	1	1	1	1	1
9	1	1	1	1	1
10	1	1	1	1	1
11	1	1	1	1	1
12	1	1	1	1	1
13	1	1	1	1	1
14	1	1	1	1	1
15	1	1	1	1	1
16	1	1	1	1	1
17	1	1	1	1	1
18	1	1	1	1	1
19	1	1	1	1	1
20	1	1	1	1	1
21	1	1	1	1	1
22	1	1	1	1	1
23	1	1	1	1	1
24	1	1	1	1	1
25	1	1	1	1	1
26	1	1	1	1	1
27	1	1	1	1	1
28	1	1	1	1	1
29	1	1	1	1	1
30	1	1	1	1	1
31	1	1	1	1	1
32	1	1	1	1	1
33	1	1	1	1	1
34	1	1	1	1	1
35	1	1	1	1	1
36	1	1	1	1	1
37	1	1	1	1	1
38	1	1	1	1	1
39	1	1	1	1	1
40	1	1	1	1	1
41	1	1	1	1	1
42	1	1	1	1	1
43	1	1	1	1	1
44	1	1	1	1	1
45	1	1	1	1	1
46	1	1	1	1	1
47	1	1	1	1	1
48	1	1	1	1	1
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50	1	1	1	1	1
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52	1	1	1	1	1
53	1	1	1	1	1
54	1	1	1	1	1
55	1	1	1	1	1
56	1	1	1	1	1
57	1	1	1	1	1
58	1	1	1	1	1
59	1	1	1	1	1
60	1	1	1	1	1
61	1	1	1	1	1
62	1	1	1	1	1
63	1	1	1	1	1
64	1	1	1	1	1
65	1	1	1	1	1
66	1	1	1	1	1
67	1	1	1	1	1
68	1	1	1	1	1
69	1	1	1	1	1
70	1	1	1	1	1
71	1	1	1	1	1
72	1	1	1	1	1
73	1	1	1	1	1
74	1	1	1	1	1
75	1	1	1	1	1
76	1	1	1	1	1
77	1	1	1	1	1
78	1	1	1	1	1
79	1	1	1	1	1
80	1	1	1	1	1
81	1	1	1		